FIG. 1A

```
Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

GTCGACCCACGCGTCCGCACTCAACAATGCCTGCCCCTCTCTGACTGCACCGTCCCGCCGCCGCTGCCGCCGCCGCGCC  79

CAAGCCAAGTCGAGCGGGGGCGTTGCCCACCGACGGCACAGCCCTTGGGCCCGCCCGGGACCAGGAGGTGAGCCGCGCG  158

                                                            M   H   S   P      4
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCCGCAGCCCGCCGCCGAG ATG CAC AGC CCG    233

 P   G   L   L   A   L   W   L   C   A   V   L   C   A   S   A   R   G   G   S      24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGG GGC AGC    293

 D   P   Q   P   G   P   G   R   P   A   C   P   A   P   C   H   C   Q   E   D      44
GAC CCC CAG CCT GGC CCG GGG CGT CCC GCC TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC    353

 G   I   M   L   S   A   D   C   S   E   L   G   L   S   V   V   P   A   D   L      64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG    413

 D   P   L   T   A   Y   L   D   L   S   M   N   N   L   T   E   L   Q   P   G      84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT    473

 L   F   H   H   L   R   F   L   E   E   L   R   L   S   G   N   H   L   S   H     104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC    533

 I   P   G   Q   A   F   S   G   L   H   S   L   K   I   L   M   L   Q   S   N     124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC    593
```

FIG.1B

```
Q   L   R   G   I   P   A   E   A   L   W   E   L   P   S   L   Q   S   L   R    144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC  653

L   D   A   N   L   I   S   L   V   P   E   R   S   F   E   G   L   S   S   L    164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC  713

R   H   L   W   L   D   D   N   A   L   T   E   I   P   V   R   A   L   N   N    184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC  773

L   P   A   L   Q   A   M   T   L   A   L   N   H   I   R   H   I   P   D   Y    204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT  833

A   F   Q   N   L   T   S   L   V   V   L   H   L   H   N   N   R   I   Q   H    224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT  893

V   G   T   H   S   F   E   G   L   H   N   L   E   T   L   D   L   N   Y   N    244
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAC TAT AAT  953

E   L   Q   E   F   P   L   A   I   R   T   L   G   R   L   Q   E   L   G   F    264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC  1013

H   N   N   N   I   K   A   I   P   E   K   A   F   M   G   N   P   L   L   Q    284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG  1073

T   I   H   F   Y   D   N   P   I   Q   F   V   G   R   S   A   F   Q   Y   L    304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG  1133
```

FIG. 1C

```
 S   K   L   H   T   L   S   L   N   G   A   T   D   I   Q   E   F   P   D   L    324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC  1193

 K   G   T   T   S   L   E   I   L   T   L   T   R   A   G   I   R   L   L   P    344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA  1253

 P   G   V   C   Q   Q   L   P   R   L   R   I   L   E   L   S   H   N   Q   I    364
CCG GGA GTG TGC CAA CAG CTG CCT AGG CTC CGA ATC CTG GAG CTG TCT CAT AAT CAG ATC  1313

 E   E   L   P   S   L   H   R   C   Q   K   L   E   E   I   G   L   R   H   N    384
GAG GAG TTA CCC AGC CTG CAC AGA TGT CAG AAG CTG GAG GAA ATT GGC CTC CGA CAT AAC  1373

 R   I   K   E   I   G   A   D   T   F   S   Q   L   G   S   L   Q   A   L   D    404
AGG ATC AAG GAA ATT GGT GCA GAT ACC TTC AGC CAG CTG GGC TCC TTG CAA GCT TTA GAC  1433

 L   S   W   N   A   I   R   A   I   H   P   E   A   F   S   T   L   R   S   L    424
CTG AGT TGG AAT GCC ATC CGT GCC ATC CAC CCT GAG GCT TTC TCA ACC CTT CGA TCC TTG  1493

 V   K   L   D   L   T   D   N   Q   L   T   T   L   P   L   A   G   L   G   G    444
GTT AAG CTG GAC CTG ACT GAC AAC CAG CTG ACC ACA CTG CCC CTG GCT GGG CTG GGA GGC  1553

 L   M   H   L   K   L   K   G   N   L   A   L   S   Q   A   F   S   K   D   S    464
CTG ATG CAC CTG AAG CTC AAA GGG AAC TTG GCC CTG TCT CAG GCC TTC TCC AAG GAC AGT  1613

 F   P   K   L   R   I   L   E   V   P   Y   A   Y   Q   C   C   A   Y   G   I    484
TTC CCA AAA CTG AGG ATC CTG GAG GTG CCC TAC GCC TAC CAG TGC TGT GCC TAC GGC ATC  1673
```

FIG.1D

```
 C   A   S   F   F   K   T   S   G   Q   W   Q   A   E   D   F   H   P   E   E    504
TGT GCC AGC TTC TTC AAG ACC TCT GGG CAG TGG CAG GCC GAG GAC TTT CAT CCA GAA GAA  1733

 E   E   A   P   K   R   P   L   G   L   L   A   G   Q   A   E   N   H   Y   D    524
GAG GAG GCA CCA AAG AGG CCC CTG GGT CTC CTT GCT GGA CAA GCT GAG AAC CAC TAT GAC  1793

 L   D   L   D   E   L   Q   M   G   T   E   D   S   K   P   N   P   S   V   Q    544
CTA GAC CTG GAT GAG CTC CAG ATG GGG ACA GAG GAC TCA AAG CCA AAC CCC AGT GTC CAG  1853

 C   S   P   V   P   G   P   F   K   P   C   E   H   L   F   E   S   W   G   I    564
TGC AGC CCT GTT CCA GGC CCC TTC AAG CCC TGC GAG CAC CTC TTT GAG AGC TGG GGC ATC  1913

 R   L   A   V   W   A   I   V   L   L   S   V   L   C   N   G   L   V   L   L    584
CGC CTT GCT GTG TGG GCC ATC GTG CTG CTC TCC GTA CTC TGT AAC GGG CTG GTG CTG CTG  1973

 T   V   F   A   S   G   P   S   P   L   S   P   V   K   L   V   V   G   A   M    604
ACA GTC TTT GCC AGC GGA CCC AGC CCG CTG TCC CCC GTC AAG CTT GTG GTG GGT GCG ATG  2033

 A   G   A   N   A   L   T   G   I   S   C   G   L   L   A   S   V   D   A   L    624
GCA GGC GCC AAC GCC CTG ACG GGC ATT TCC TGT GGT CTC CTG GCC TCT GTG GAC GCC TTG  2093

 T   Y   G   Q   F   A   E   Y   G   A   R   W   E   S   G   L   G   C   Q   A    644
ACC TAT GGT CAG TTC GCT GAG TAT GGA GCC CGC TGG GAG AGC GGT CTG GGC TGC CAG GCT  2153

 T   G   F   L   A   V   L   G   S   E   A   S   V   L   L   L   T   L   A   A    664
ACG GGC TTC CTG GCT GTC CTG GGT TCA GAG GCG TCG GTG CTG CTG CTC ACA CTG GCG GCC  2213
```

FIG. 1E

```
 V   Q   C   S   I   S   V   T   C   V   R   A   Y   G   K   A   P   S   P   G    684
GTG CAG TGC AGC ATC TCT GTG ACC TGC GTC CGA GCC TAC GGG AAG GCG CCG TCG CCT GGC  2273

 S   V   R   A   G   A   L   G   C   L   A   L   A   G   L   A   A   A   L   P    704
AGC GTC CGC GCA GGC GCA CTG GGA TGC CTG GCG CTG GCC GGG CTG GCC GCA GCA CTG CCG  2333

 L   A   S   V   G   E   Y   G   A   S   P   L   C   L   P   Y   A   P   P   E    724
CTG GCC TCG GTG GGA GAG TAT GGC GCC TCC CCA CTC TGC CTG CCC TAC GCC CCA CCC GAG  2393

 G   R   P   A   A   L   G   F   A   V   A   L   V   M   M   N   S   L   C   F    744
GGC CGG CCG GCC GCC CTG GGC TTC GCT GTA GCC CTG GTG ATG ATG AAC TCG CTC TGC TTC  2453

 L   V   V   A   G   A   Y   I   K   L   Y   C   D   L   P   R   G   D   F   E    764
CTG GTG GTG GCC GGC GCC TAC ATC AAG CTC TAC TGT GAC CTG CCA CGG GGT GAC TTT GAG  2513

 A   V   W   D   C   A   M   V   R   H   V   A   W   L   I   F   A   D   G   L    784
GCC GTG TGG GAC TGC GCC ATG GTG CGC CAC GTG GCC TGG CTC ATC TTT GCA GAT GGC CTC  2573

 L   Y   C   P   V   A   F   L   S   F   A   S   M   L   G   L   F   P   V   T    804
CTC TAC TGC CCC GTG GCC TTC CTC AGC TTT GCC TCC ATG CTG GGC CTC TTC CCT GTC ACC  2633

 P   E   A   V   K   S   V   L   L   V   V   L   P   L   P   A   C   L   N   P    824
CCC GAG GCT GTC AAG TCA GTC CTT CTG GTG GTG CTG CCT CTG CCT GCC TGC CTC AAC CCA  2693

 L   L   Y   L   L   F   N   P   H   F   R   D   D   L   R   R   L   W   P   S    844
CTG CTC TAC CTG CTC TTC AAC CCT CAC TTC CGG GAT GAC CTT CGG CGG CTC TGG CCA AGC  2753
```

FIG. 1F

```
 P   R   S   P   G   P   L   A   Y   A   A   A   G   E   L   E   K   S   S   C     864
CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC   2813

 D   S   T   Q   A   L   V   A   F   S   D   V   D   L   I   L   E   A   S   E     884
GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG   2873

 A   G   Q   P   P   G   L   E   T   Y   G   F   P   S   V   T   L   I   S   R     904
GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA   2933

 H   Q   P   G   A   T   R   L   E   G   N   H   F   I   E   S   D   G   T   K     924
CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG   2993

 F   G   N   P   Q   P   P   M   K   G   E   L   L   L   K   A   E   G   A   T     944
TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT   3053

 L   A   G   C   G   S   S   V   G   G   A   L   W   P   S   G   S   L   F   A     964
TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC   3113

 S   H   L   *                                                                     968
TCT CAC TTG TAA                                                                   3125

ATATCCCTCTCTGTTTGTCCTCTCCCCATCCAATGATGGCTGCTTATAAAAGAAAGACAACTCCAACTCCATAGCAAGA   3204

TGGCCAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGTCTTGG   3283

CCTTCAGCTTCACTTTCACCCTGGGCCTTCTCTGTCCAATCCAATACTTCTGACAGAGGCCTGGGAAATTTGCATAGGA   3362
```

FIG.1G

GAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGAG 3441

GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTGTGACATATAGAATATAAAATG 3520

TGTTCTGCGTTCCATTAATCTTGACCTATGCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA 3599

AAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637
??

FIG. 2A

```
LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+
 ftmzb048h1
           67 LTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH    114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p+++f++L+
 ftmzb048h1
          115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +L++L+L++N Lt++p  al+nLp L+   L  N+++++p+++fqnL+
 ftmzb048h1
          163 SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL k<-*
              +L +L+L nN+++++  +++++L+nLe+LdL++N+L+++p  + + L+
 ftmzb048h1
          211 SLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFPL-AIRTLG 257
```

FIG.2B

```
LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ +  ++fq L+
 ftmzb048h1
      258    RLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
           *->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppglfqn Lk<-*
              +L++L+L++  +++++p+  l++ ++Le L L +  ++ lppg++q L+
 ftmzb048h1
      306    KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +L+ L+Ls+N++++lp+  l+ +++Lee+ L +N+++++  ++f+ L+
 ftmzb048h1
      353    RLRILELSHNQIEELPS--LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
           *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
              +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp   + +L
 ftmzb048h1
       399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446
```

FIG. 3A-1

Protein (species)*	Function-lgand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α2-GP (human)	?-?	Serum
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm
U2 snRNP A′ (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin,TGF-β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP lb	PM (EC)
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC
IpaH7.8 (Shigella flexnen)	?-?	?
IpaH4.5 (Shigella flexnen)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence	PIR entry
		5 10 15 20 25	
15	28 (A)	.LE.L.L..C-.LT...C..L..aL....	A31857
	29 (B)	.L.EL.L..N-.LGD.Ga..L...L..P..	
8	24	.L..L.L..N-.L..-L...LL...--.	NBHUA2
8	29	.L..L.L..N-.a.......a..a......	BVBYN1
4	24	.L..L.a..N-.a..-........L--.	S03616
8	24	.L..L.L..N-.I..-a....a...--.	A40757
10	24	.L..L.L..N-.I..-V....a...--.	NBHUC8
11	24	.L..L.L..N-.a..-a....a...--.	S05390
12	24	.L..L.L..N-.L..-.....a...--.	A41748
6	24	.L..a.L..N-.I..-.....a...--.	A41781
6	24	.L..a.L..N-.a..-.....F...--.	A35272
7	24	.L..L.L..N-.L..-LP.GL...L--.	NBHUIA
14	24	.L..L.L..N-.L..-LP..LF..L--.	-
12	20	.L..L.a..N-.L..-LP-.----L--PP	A33950
6	20	.L..L.V..N-.L..-LP-.----L--P.	A35149
8	20	.L..L.a..N-.L..-LP-.----L--P.	S18248
19	24	.L..L.L..N-.L..-.....F...--.	A29943
19	24	.L..L.L..N-.I..-.....F..L--.	A36665
7	24	.L..LNL..N-.I..-a...aF..L--.	S28464
30	24	.L..L.L..N-.a..-a....F..a--.	A29944
16	23	.L..L.LS.N-.L..-aP..a..-L--.	-
8	24	.L..L.LSNN-.a..-a.......L--.	A34210

FIG. 3B-1

Protein (species)*	Function-lgand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylate cyclase (Saccharomyces Cerevisiae)	Signal transduction-RAS	PM (cytoplasm)
T-LR (Tyrpanosoma brucel)	?-?	?
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?
DRT100 (Arabidopsis thallana)	Recombination-?	Chloroplast
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus
p34 ribosome-binding protein(rat)	RM membranes-ribosome	RM membrane (cytoplasm)
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma
Intermalin (Listeria monocytogenes)	Invasion-?	Cell wall
InIB (Listeria monocytogenes)	?-?	?

LRR superfamily

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L.L..N-.................	TDHUM4
2	23	.L..L.LS.N-.L....-.-....--.	TVHUTT
3	23	.L..L.aT.N-.LTS...-.-....--T	S06943
3	23	.LR.aNLSQN-.L...S.-.-....--.	A40026
11	23	.L..a.L..N-...G.aP-.-a.SL--.	JQ1674
5	25	.L..L.a..T-.a........F...--.	A41343
7	25	.L..L.aS.T-.....LP...a..a--.	A34548
6	25	.a..L.a.NN..a.S-a....a...--.	A40077
20	23	.L..L.L..N-.a..-a...-a..L--.	OYBY
18	23	.L..L.LSGC..a..--a..-a..L--.	A36359
3	23	.a.LaDI..N--LP..a......N---.	DDBYD1
5	26	.L..L.a..C..a....a...a...--P	A25226
5	24	.L..LNL..N-.L.G.IP.S-a.S.--.	A46260
9	26	.L..a.L..C.NaTD..a..-L..L.-.	A41529
4	23	.L..L.a..N-.LT.-LP.E-a...--.	S31286
11	22	.L..L.a..N-.I..-a--ENa..L--.	A38439
4	24	.L..LDL..N-.L..-LP...F..L--.	-
12	24	.L..L.L..N-.L..-LP..aF..L--.	A34901
13	22	NL..L.L..n-QISDI.P---L..L--T	A39930
6	22	.L..L.L..N-.L.DI..---L..L--.	C39930
		5 10 15 20 25	
		.L..L.L..N*.a..*a****a**a**.**	

FIG. 4

>human DNA seq.
TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCG
AGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGA
CCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAATT

FIG. 5

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLR
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

FIG. 6

```
LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11
            *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
               +L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp   + +L
    fahr   64  SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

            k<-*

    fahr  111 M    111
```

FIG. 7A

```
                     1                                                                              80
ftmzb048h10          MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNNLTE
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                     81                                                                            160
ftmzb048h10          LQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEG
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                     161                                                                           240
ftmzb048h10          LSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLD
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                     241                                                                           320
ftmzb048h10          LNYNELQEFPLAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLSKLHTLSLNGATDIQE
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~NTTHYRES------WYACRYRS-----GIPGST----
                     321                                                                           400
ftmzb048h10          FPDLKGTTSLEILTLTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
fahr_human           ----H--ASVE-----RSQGLSLP----AHPASLAALAASNTTASG--------KLEX------------DTFSQLSSL
                     401                                                                           480
ftmzb048h10          QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
Aa_of_aambb001d112   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
Fahr_human           QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCC
                     481                                                                           560
ftmzb048h10          AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPGPFKPCEHLFE
Aa_of_aambb001d112   AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPHPSVQCSPVPGPFKPCEHLFE
fahr_human           PYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFE
```

FIG. 7B

```
                    561                                                                              640
ftmzb048h10         SWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
Aa_of_aambb001d112  SWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLVVGAMAGANALSGISCGLLASVDALTYGQFAEYGARWESGL
fahr_human          SWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGL
                                 I                              TM II

                    641                                                                              720
ftmzb048h10         GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
Aa_of_aambb001d112  GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
fahr_human          GCRATGFLAVLGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPY
                             TM III                                  TM IV

                    721                                                                              800
ftmzb048h10         APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
Aa_of_aambb001d112  APPEGRPAALGFAVALVMMNSLCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
fahr_human          APPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL
                                 TM V                                           TM VI

                    801                                                                              880
ftmzb048h10         FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
Aa_of_aambb001d112  FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
fahr_human          FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
                                 TM VII

                    881                                                                              960
ftmzb048h10         EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG
Aa_of_aambb001d112  EASEAGQPPGLETYGFPSVTLISRHQPGATRLEGNHFVESDGTKFGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG
fahr_human          EASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGLSGGGGFQPSG
                    961                                                                              968
ftmzb048h10         SLFASHLN
Aa_of_aambb001d112  SLFASHLN
fahr_human          LAFASHVN
```

FIG.8A

```
 G   L   H   N   L   E   T   L   D   L   N   Y   N   K   L   Q   E   F   P   V    20
GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAT TAT AAC AAG CTG CAG GAG TTC CCT GTG   60

 A   I   R   T   L   G   R   L   Q   E   L   G   F   H   N   N   N   I   K   A    40
GCC ATC CGG ACC CTG GGC AGA CTG CAG GAA CTG GGG TTC CAT AAC AAC AAC ATC AAG GCC  120

 I   P   E   K   A   F   M   G   N   P   L   L   Q   T   I   H   F   Y   D   N    60
ATC CCA GAA AAG GCC TTC ATG GGG AAC CCT CTG CTA CAG ACG ATA CAC TTT TAT GAT AAC  180

 P   I   Q   F   V   G   R   S   A   F   Q   Y   L   P   K   L   H   T   L   S    80
CCA ATC CAG TTT GTG GGA AGA TCG GCA TTC CAG TAC CTG CCT AAA CTC CAC ACA CTA TCT  240

 L   N   G   A   M   D   I   Q   E   F   P   D   L   K   G   T   T   S   L   E   100
CTG AAT GGT GCC ATG GAC ATC CAG GAG TTT CCA GAT CTC AAA GGC ACC ACC AGC CTG GAG  300

 I   L   T   L   T   R   A   G   I   R   L   L   P   S   G   M   C   Q   Q   L   120
ATC CTG ACC CTG ACC CGC GCA GGC ATC CGG CTG CTC CCA TCG GGG ATG TGC CAA CAG CTG  360

 P   R   L   R   V   L   E   L   S   H   N   Q   I   E   E   L   P   S   L   H   140
CCC AGG CTC CGA GTC CTG GAA CTG TCT CAC AAT CAA ATT GAG GAG CTG CCC AGC CTG CAC  420

 R   C   Q   K   L   E   E   I   G   L   Q   H   N   R   I   W   E   I   G   A   160
AGG TGT CAG AAA TTG GAG GAA ATC GGC CTC CAA CAC AAC CGC ATC TGG GAA ATT GGA GCT  480

 D   T   F   S   Q   L   S   S   L   Q   A   L   D   L   S   W   N   A   I   R   180
GAC ACC TTC AGC CAG CTG AGC TCC CTG CAA GCC CTG GAT CTT AGC TGG AAC GCC ATC CGG  540
```

FIG.8B

```
S   I   H   P   E   A   F   S   T   L   H   S   L   V   K   L   D   L   T   D    200
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC  600

N   Q   L   T   T   L   P   L   A   G   L   G   G   L   M   H   L   K   L   K    220
AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA  660

G   N   L   A   L   S   Q   A   F   S   K   D   S   F   P   K   L   R   I   L    240
GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG  720

E   V   P   Y   A   Y   Q   C   C   P   Y   G   M   C   A   S   F   F   K   A    260
GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC  780

S   G   Q   W   E   A   E   D   L   H   L   D   D   E   E   S   S   K   R   P    280
TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG GAG TCT TCA AAA AGG CCC  840

L   G   L   L   A   R   Q   A   E   N   H   Y   D   Q   D   L   D   E   L   Q    300
CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG GAC CTG GAT GAG CTC CAG  900

L   E   M   E   D   S   K   P   H   P   S   V   Q   C   S   P   T   P   G   P    320
CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC  960

F   K   P   C   E   Y   L   F   E   S   W   G   I   R   L   A   V   W   A   I    340
TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GCC GTG TGG GCC ATC  1020

V   L   L   S   V   L   C   N   G   L   V   L   L   T   V   F   A   G   G   P    360
GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG CTG ACC GTG TTC GCT GGC GGG CCT  1080
```

FIG. 8C

```
 A   P   L   P   P   V   K   F   V   V   G   A   I   A   G   A   N   T   L   T    380
GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT  1140

 G   I   S   C   G   L   L   A   S   V   D   A   L   T   F   G   Q   F   S   E    400
GGC ATT TCC TGT GGC CTT CTA GCC TCA GTC GAT GCC CTG ACC TTT GGT CAG TTC TCT GAG  1200

 Y   G   A   R   W   E   T   G   L   G   C   R   A   T   G   F   L   A   V   L    420
TAC GGA GCC CGC TGG GAG ACG GGG CTA GGC TGC CGG GCC ACT GGC TTC CTG GCA GTA CTT  1260

 G   S   E   A   S   V   L   L   L   T   L   A   A   V   Q   C   S   V   S   V    440
GGG TCG GAG GCA TCG GTG CTG CTG CTC ACT CTG GCC GCA GTG CAG TGC AGC GTC TCC GTC  1320

 S   C   V   R   A   Y   G   K   S   P   S   L   G   S   V   R   A   G   V   L    460
TCC TGT GTC CGG GCC TAT GGG AAG TCC CCC TCC CTG GGC AGC GTT CGA GCA GGG GTC CTA  1380

 G   C   L   A   L   A   G   L   A   A   A   L   P   L   A   S   V   G   E   Y    480
GGC TGC CTG GCA CTG GCA GGG CTG GCC GCC GCA CTG CCC CTG GCC TCA GTG GGA GAA TAC  1440

 G   A   S   P   L   C   L   P   Y   A   P   P   E   G   Q   P   A   A   L   G    500
GGG GCC TCC CCA CTC TGC CTG CCC TAC GCG CCA CCT GAG GGT CAG CCA GCA GCC CTG GGC  1500

 F   T   V   A   L   V   M   M   N   S   F   C   F   L   V   V   A   G   A   Y    520
TTC ACC GTG GCC CTG GTG ATG ATG AAC TCC TTC TGT TTC CTG GTC GTG GCC GGT GCC TAC  1560

 I   K   L   Y   C   D   L   P   R   G   D   F   E   A   V   W   D   C   A   M    540
ATC AAA CTG TAC TGT GAC CTG CCG CGG GGC GAC TTT GAG GCC GTG TGG GAC TGC GCC ATG  1620
```

FIG. 8D

```
V   R   H   V   A   W   L   I   F   A   D   G   L   L   Y   C   P   V   A   F    560
GTG AGG CAC GTG GCC TGG CTC ATC TTC GCA GAC GGG CTC CTC TAC TGT CCC GTG GCC TTC 1680

L   S   F   A   S   M   L   G   L   F   P   V   T   P   E   A   V   K   S   V    580
CTC AGC TTC GCC TCC ATG CTG GGC CTC TTC CCT GTC ACG CCC GAG GCC GTC AAG TCT GTC 1740

L   L   V   V   L   P   L   P   A   C   L   N   P   L   L   Y   L   L   F   N    600
CTG CTG GTG GTG CTG CCC CTG CCT GCC TGC CTC AAC CCA CTG CTG TAC CTG CTC TTC AAC 1800

P   H   F   R   D   D   L   R   R   L   R   P   R   A   G   D   S   G   P   L    620
CCC CAC TTC CGG GAT GAC CTT CGG CGG CTT CGG CCC CGC GCA GGG GAC TCA GGG CCC CTA 1860

A   Y   A   A   A   G   E   L   E   K   S   S   C   D   S   T   Q   A   L   V    640
GCC TAT GCT GCG GCC GGG GAG CTG GAG AAG AGC TCC TGT GAT TCT ACC CAG GCC CTG GTA 1920

A   F   S   D   V   D   L   I   L   E   A   S   E   A   G   R   P   P   G   L    660
GCC TTC TCT GAT GTG GAT CTC ATT CTG GAA GCT TCT GAA GCT GGG CGG CCC CCT GGG CTG 1980

E   T   Y   G   F   P   S   V   T   L   I   S   C   Q   Q   P   G   A   P   R    680
GAG ACC TAT GGC TTC CCC TCA GTG ACC CTC ATC TCC TGT CAG CAG CCA GGG GCC CCC AGG 2040

L   E   G   S   H   C   V   E   P   E   G   N   H   F   G   N   P   Q   P   S    700
CTG GAG GGC AGC CAT TGT GTA GAG CCA GAG GGG AAC CAC TTT GGG AAC CCC CAA CCC TCC 2100

M   D   G   E   L   L   L   R   A   E   G   S   T   P   A   G   G   G   L   S    720
ATG GAT GGA GAA CTG CTG CTG AGG GCA GAG GGA TCT ACG CCA GCA GGT GGA GGC TTG TCA 2160
```

FIG. 8E

```
 G   G   G   G   F   Q   P   S   G   L   A   F   A   S   H   V   *      737
GGG GGT GGC GGC TTT CAG CCC TCT GGC TTG GCC TTT GCT TCA CAC GTG TAA    2211

ATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACA  2290

AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA  2369

CCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG  2448

TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGG  2527

TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGACTCATG  2606

GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTT  2685

TGGAAGAGATTAAAAAAAAAAAAAAA                                                       2711
```

FIG. 9

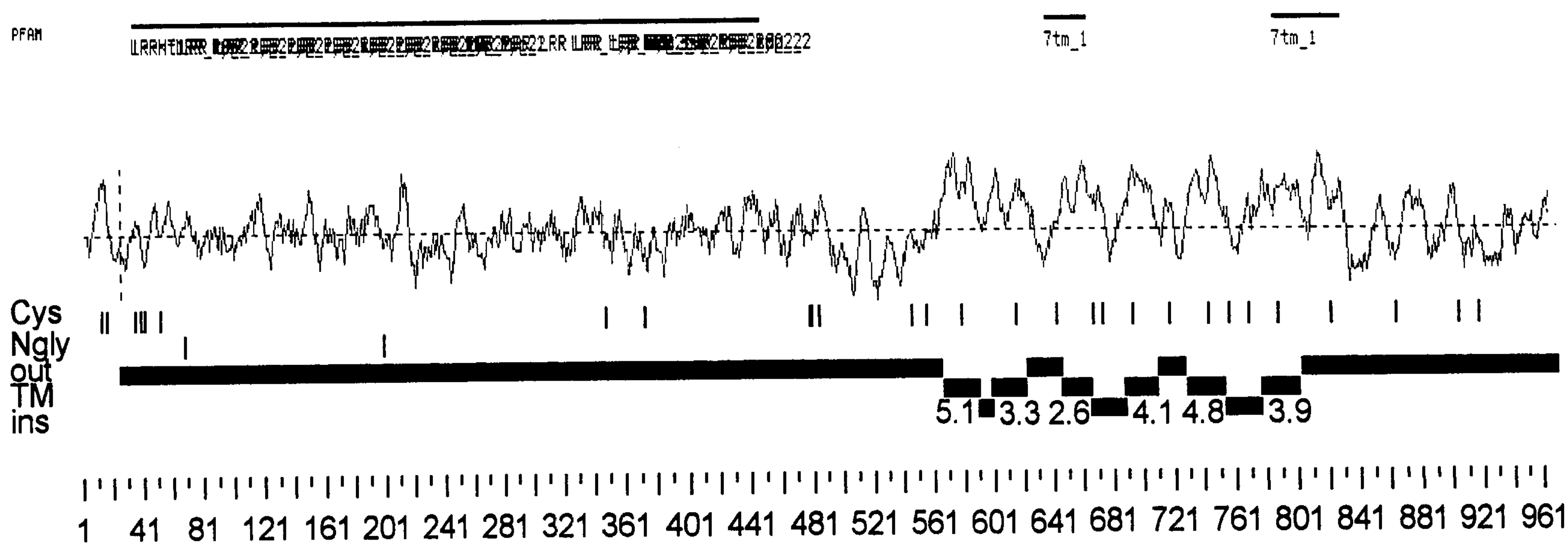
PFAM
7tm_1
7tm_1
Cys
Ngly
out
TM
ins
5.1
3.3
2.6
4.1
4.8
3.9
1 41 81 121 161 201 241 281 321 361 401 441 481 521 561 601 641 681 721 761 801 841 881 921 961

FIG. 10A

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)

- -

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

- -

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR	Leucine Rich Repeat	241.4	1.3e-68	16
LRRNT	Leucine rich repeat N-terminal domain	27.2	0.00038	1
7tm_1	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
LRRNT	1/1	34	65	..	1	31	[]	27.2	0.00038
LRR	1/16	67	90	..	1	23	[]	12.4	11
LRR	2/16	91	114	..	1	23	[]	24.2	0.0031
LRR	3/16	115	138	..	1	23	[]	19.9	0.062
LRR	4/16	139	162	..	1	23	[]	16.4	0.7
LRR	5/16	163	186	..	1	23	[]	27.5	0.00031
LRR	6/16	187	210	..	1	23	[]	12.1	13
LRR	7/16	211	234	..	1	23	[]	21.6	0.019
LRR	8/16	235	257	..	1	23	[]	18.2	0.2
LRR	9/16	258	281	..	1	23	[]	19.0	0.11
LRR	10/16	282	305	..	1	23	[]	10.2	32
LRR	11/16	306	328	..	1	23	[]	5.6	1.5e+02
LRR	12/16	329	352	..	1	23	[]	8.8	52
LRR	13/16	353	374	..	1	23	[]	19.2	0.097
LRR	14/16	375	398	..	1	23	[]	16.9	0.49
LRR	15/16	399	422	..	1	23	[]	23.7	0.0042
LRR	16/16	423	446	..	1	23	[]	16.4	0.66
7tm_1	1/2	635	662	..	51	79	..	3.4	2.2
7tm_1	2/2	784	827	..	207	259	.]	1.1	11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

```
                   *->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-*
                      aCp++C+C +++  l+ dCs++gL  +vP dl
   15088    34     ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD     65
```

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                        +LdLs N+Lt+l pglf++L+
   15088    67     LTAYLDLSMNnLTELQPGLFHHLR     90
```

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                      LeeL+Ls+N+L+++p  +fs+L
   15088    91     FLEELRLSGNhLSHIPGQAFSGLY     114
```

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                      +L+ L L+nN+L ++p +++  Lp
   15088    115    SLKILMLQNNqLGGIPAEALWELP     138
```

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                      +L++L+L+ N ++ +p+ +f++L+
   15088    139    SLQSLRLDANlISLVPERSFEGLS     162
```

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                      +L++L+L++N Lt++p  +++nLp
   15088    163    SLRHLWLDDNaLTEIPVRALNNLP     186
```

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                       L+   L  N+++++p+ +f+nL+
   15088    187    ALQAMTLALNrISHIPDYAFQNLT     210
```

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

```
                   *->nLeeLdLsnN.LtslppglfsnLp<-*
                      +L +L+L+nN++++l  ++f++L
   15088    211    SLVVLHLHNNrIQHLGTHSFEGLH     234
```

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    nLe+LdL++N+L+++p  +++ L
  15088   235    NLETLDLNYNkLQEFPV-AIRTLG    257
```

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    +L+eL ++nN+++ +p+++f + p
  15088   258    RLQELGFHNNnIKAIPEKAFMGNP    281
```

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                     L+++++ +N+++ +  ++f+ Lp
  15088   282    LLQTIHFYDNpIQFVGRSAFQYLP    305
```

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
```
                 *->nLeeLdLsnN..LtslppglfsnLp<-*
                    +L++L+L++  +++++p+  +++ +
  15088   306    KLHTLSLNGAmdIQEFPD--LKGTT    328
```

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    +Le L L + +++ lp+g +++Lp
  15088   329    SLEILTLTRAgIRLLPSGMCQQLP    352
```

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    +L++L Ls+N++++lp+  ++ ++
  15088   353    RLRVLELSHNqIEELPS--LHRCQ    374
```

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    +Lee+ L++N++ ++  ++fs+L+
  15088   375    KLEEIGLQHNrIWEIGADTFSQLS    398
```

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
```
                 *->nLeeLdLsnN.LtslppglfsnLp<-*
                    +L+ LdLs N ++s++p++fs L
  15088   399    SLQALDLSWNaIRSIHPEAFSTLH    422
```

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FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

```
                *->nLeeLdLsnN.LtslppglfsnLp<-*
                   +L +LdL +N+Lt+lp   + +L
    15088   423    SLVKLDLTDNqLTTLPLAGLGGLM    446
```

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

```
                *->dWpfGsalCklvtaldvvnmyaSillLta<-*
                   +W  G ++C+ +++l v+ + aS+llLt+
    15088   635    RWETG-LGCRATGFLAVLGSEASVLLLTL    662
```

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

```
                *->lCWlPyfivllldtlc.lsiimsstCelervlptallvtlwLayvNs
                   l+  P + + +  +l  ++          +++++++v l++  + +
    15088   784    LLYCPVAFLSFASMLGlFPV----------
TPEAVKSVLLVVLPLPA 820

                clNPiIY<-*
                clNP++Y
    15088   821 CLNPLLY    827
```

FIG. 11A

```
//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                  /ddm/robison/smart/smart/smart.all.hmms
Sequence file:             /prod/ddm/wspace/orfanal/oa-script.12184.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
```

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrnt1		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
lrrnt1	1/1	34	70	..	1	38	[]	25.7	0.0011
LRR_PS_2	1/13	64	87	..	1	24	[]	1.9	1.2e+02
LRR_typ_2	1/14	64	88	..	1	24	[]	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	20	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	0.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350	..	1	24	[]	3.1	29
LRR_bac_2	6/7	351	370	..	1	20	[]	14.6	1.3
LRR_PS_2	10/13	351	372	..	1	24	[]	10.8	8
LRR_sd22_2	3/5	351	372	..	1	22	[]	7.6	16
LRR_typ_2	11/14	351	373	..	1	24	[]	18.8	0.13
LRR_RI_2	4/4	351	378	..	1	28	[]	2.6	19
LRR_PS_2	11/13	373	396	..	1	24	[]	2.3	1e+02
LRR_typ_2	12/14	374	396	..	1	24	[]	6.8	10
LRR_sd22_2	4/5	397	418	..	1	22	[]	7.0	19
LRR_PS_2	12/13	397	419	..	1	24	[]	13.6	3.4
LRR_typ_2	13/14	397	420	..	1	24	[]	30.4	4.3e-05
LRR_bac_2	7/7	421	440	..	1	20	[]	5.8	18
LRR_sd22_2	5/5	421	441	..	1	22	[]	3.7	49
LRR_PS_2	13/13	421	442	..	1	24	[]	5.5	39
LRR_typ_2	14/14	421	444	..	1	24	[]	21.6	0.018

Alignments of top-scoring domains:

lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011

```
                *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
                   +CPapC+C ++    ++ dCs++gL   +vP dl + t +
   15088    34     ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDPLTAY    70
```

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02

```
                *->LtsL.qvLdLsnNnLsGeIPsslgn<-*
                   L  L+ +LdLs NnL+ e+ + l+
   15088    64     LDPLtAYLDLSMNNLT-ELQPGLFH    87
```

FIG. 11D

```
LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
                   *->LpnL.reLdLsnNqLtsLPpgaFqg<-*
                      L  L+  LdLs N+Lt+L pg+F++
       15088    64    LDPLtAYLDLSMNNLTELQPGLFHH    88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
                   *->PpsLkeLnvsnNrLteLPeL<-*
                        +L+eL+ s+N+L+  P
       15088    89    LRFLEELRLSGNHLSHIPGQ    108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+ L++L+Ls+N+Ls +IP + ++
       15088    89    LRFLEELRLSGNHLS-HIPGQAFS    111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L+ L+eL+Ls+N+L+++P +aF+g
       15088    89    LRFLEELRLSGNHLSHIPGQAFSG    112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
                   *->npsLreLdLsnNkl.gdeGaraLaeaLks<-*
                      ++ L+eL+Ls+N+l+++ G  +  ++L s
       15088    89    LRFLEELRLSGNHLsHIPG--QAFSGLYS    115
```

FIG. 11E

```
LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
                   *->PpsLkeLnvsnNrLteLPeL<-*
                        sLk+L  +nN+L   P+
       15088   113    LYSLKILMLQNNQLGGIPAE    132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L sL++L L+nN+L G   + l+
       15088   113    LYSLKILMLQNNQLGGIPAEALWE    136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L +L+ L L+nNqL  +P++a++
       15088   113    LYSLKILMLQNNQLGGIPAEALWE    136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
                   *->PpsLkeLnvsnNrLteLPeL<-*
                       psL++L+ + N ++  Pe
       15088   137    LPSLQSLRLDANLISLVPER    156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sLq+L+L  N +s  +P+  +
       15088   137    LPSLQSLRLDANLIS-LVPERSFE    159
```

FIG. 11F

```
LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp+L++L+L+ N ++ +P++ F+g
       15088   137    LPSLQSLRLDANLISLVPERSFEG    160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sL++L L +N L+ eIP    n
       15088   161    LSSLRHLWLDDNALT-EIPVRALN    183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++Lr+L L++N+Lt++P +a+++
       15088   161    LSSLRHLWLDDNALTEIPVRALNN    184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
                   *->LtnLeeLdLsqNkI.....kkiENLde<-*
                      L+ L++L+L +N +++ + + + NL
       15088   161    LSSLRHLWLDDNALteipvRALNNLPA    187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
                   *->npsLreLdLsnNklgdeGaraL..aeaLks<-*
                      ++sLr L+L +N l++  +raL++  aL++
       15088   161    LSSLRHLWLDDNALTEIPVRALnnLPALQA    190
```

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25

```
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+ Lq   L+ N++s +IP+  ++
   15088   185       LPALQAMTLALNRIS-HIPDYAFQ    207
```

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062

```
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     Lp+L+   L  N+++++P+ aFq+
   15088   185       LPALQAMTLALNRISHIPDYAFQN    208
```

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79

```
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     LtsL+vL+L+nN++      s+
   15088   209       LTSLVVLHLHNNRIQHLGTHSFEG    232
```

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002

```
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     L++L +L+L+nN++++L    F+g
   15088   209       LTSLVVLHLHNNRIQHLGTHSFEG    232
```

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31

```
                  *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                     ++sL +L+L nN +   G   + e+L+
   15088   209       LTSLVVLHLHNNRIQHLGTHSF-EGLHN    235
```

FIG. 11H

```
LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
                   *->LtnLeeLdLsqNkI.....kkiENLde<-*
                      Lt L++L L +N+I++ +++++E+L++
      15088   209     LTSLVVLHLHNNRIqhlgtHSFEGLHN    235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
                   *->PpsLkeLnvsnNrLteLPeL<-*
                       ++L++L+ ++N+L e+P
      15088   233     LHNLETLDLNYNKLQEFPVA    252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L+nL++LdL++N+L++ P  + +
      15088   233     LHNLETLDLNYNKLQEFPVAI-RT    255

LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L++L++LdL++N+L  e+P  +
      15088   233     LHNLETLDLNYNKLQ-EFPVAIRT    255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
                   *->PpsLkeLnvsnNrLteLPeL<-*
                        +L+eL+  nN+++  Pe
      15088   256     LGRLQELGFHNNNIKAIPEK    275
```

FIG. 11I

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85

```
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L +Lq+L ++nNn+   IP+  +
      15088   256     LGRLQELGFHNNNIK-AIPEKAFM    278
```

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026

```
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L+ L+eL  +nN+++++P+ aF g
      15088   256     LGRLQELGFHNNNIKAIPEKAFMG    279
```

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29

```
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                       ++L+ L L +  ++ LP+g++q
      15088   327     TTSLEILTLTRAGIRLLPSGMCQQ    350
```

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3

```
                   *->PpsLkeLnvsnNrLteLPeL<-*
                       p+L+ L  s+N+++eLP L
      15088   351     LPRLRVLELSHNQIEELPSL    370
```

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8

```
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L++L+vL+Ls+N++  e+Ps l +
      15088   351     LPRLRVLELSHNQIE-ELPS-LHR    372
```

FIG. 11J

```
LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L +L++L+Ls+N+I+ +  L+
       15088   351    LPRLRVLELSHNQIEELPSLHR    372

LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp Lr+L Ls+Nq+++LP  + ++
       15088   351    LPRLRVLELSHNQIEELP-SLHRC    373

LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
                   *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                      +p+Lr+L Ls+N + +    + ++ L++
       15088   351    LPRLRVLELSHNQIEELPSLHRCQKLEE    378

LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      +++L+++ L++N++     +++++
       15088   373    CQKLEEIGLQHNRIWEIGADTFSQ    396

LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                        +L+e  L++N++ ++ +++F+
       15088   374    -QKLEEIGLQHNRIWEIGADTFSQ    396
```

FIG. 11K

```
LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdLs+N I++i
       15088   397    LSSLQALDLSWNAIRSIHPEAF    418

LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sLq LdLs+N +  +I ++ ++
       15088   397    LSSLQALDLSWNAIR-SIHPEAFS    419

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++L+ LdLs+N+++s++p+aF+
       15088   397    LSSLQALDLSWNAIRSIHPEAFST    420

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
                   *->PpsLkeLnvsnNrLteLPeL<-*
                       +sL +L+  +N+Lt+LP
       15088   421    LHSLVKLDLTDNQLTTLPLA    440

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdL +N+++ +  L +
       15088   421    LHSLVKLDLTDNQLTTL-PLAG    441
```

FIG. 11L

```
LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sL+ LdL +N+L+ ++P   g
       15088   421    LHSLVKLDLTDNQLT-TLPL-AGL    442

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++L +LdL +NqLt+LP   ++g
       15088   421    LHSLVKLDLTDNQLTTLPLAGLGG    444

//
```

FIG.12A

```
GAP of: FrGcgManager_101_HTAUB3ha_  check: 2817  from: 1  to: 3637

 mLGR6 - 1 (analysis only) - Import - complete

 to: FrGcgManager_101_ITA0fLsO_  check: 3059  from: 1  to: 2711

 corrected human LGR6 (analysis o - Import - complete

 Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
 CompCheck: 8760

         Gap Weight:     12      Average Match: 10.000
      Length Weight:      4   Average Mismatch:  0.000

            Quality:  21826             Length:   3688
              Ratio:  8.051               Gaps:     20
 Percent Similarity: 84.248   Percent Identity: 84.211

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   5
                    . =   1
```

FIG. 12B

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

```
                                   .
                                   .
                                   .

                  .         .         .         .         .
 901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT 950
                   |||||||||||||||||||||||||||||||| |||
   1 ..............GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT 36
                  .         .         .         .         .
 951 AATGAGCTGCAGGAGTTCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000
     ||  ||||||||||||||||  |||| |||||||||||||||||||||||
  37 AACAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86
                  .         .         .         .         .
1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050
      ||| |||| ||||||||||||||||||||||| |||||||| || ||||
  87 GGAACTGGGGTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT 136
                  .         .         .         .         .
1051 TCATGGCAACCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC 1100
     ||||||| ||||||||| || ||||| ||||| ||||||||| ||||||||||
 137 TCATGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186
                  .         .         .         .         .
1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT 1150
     |||||||||||||| || ||||||||||||||| ||||||| || || ||
 187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236
```

FIG. 12C

```
                .         .         .         .         .
1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA 1200
     |||| ||||||||||||  || ||||| ||||| ||||| ||||||||||
 237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286

                .         .         .         .         .
1201 CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCAGACTGCTC 1250
     |||| |||||||||||||||||||||||||| || |||||| | ||||||
 287 CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC 336

                .         .         .         .         .
1251 CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
     ||| ||||  |||||||||||||||| ||||||||| ||||||| |||||
 337 CCATCGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTC 386

                .         .         .         .         .
1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
     ||| ||||| || |||||| | |||||||||||||| ||||||||  |||
 387 TCACAATCAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436

                .         .         .         .         .
1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
     ||||||| ||||||| ||| ||| | |||  ||||||||| || || |||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAATTGGAGCTGACACC 486

                :         .         .         .         .
1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
     |||||||||||| ||||| |||||||  | || || || ||||| |||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536

                .         .         .         .         .
1451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
     |||  |||||||||||||||| ||||| ||||| |  ||| |||| ||||
 537 CCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAAGC 586
```

FIG. 12D

```
                .         .         .         .         .
1501 TGGACCTGACTGACAACCAGCTGACCACACTGCCCCTGGCTGGGCTGGGA 1550
     |||||||||| |||||||||||||||||||||||||||||||| || ||
 587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGCTGGACTTGGG 636
                .         .         .         .         .
1551 GGCCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGCCTT 1600
     ||| ||||||| |||||||||||||||||| | || || || ||||||||
 637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTT 686
                .         .         .         .         .
1601 CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTACGCCT 1650
     |||||||||||||||||||||||||||||||||||||||||| || ||||
 687 CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCT 736
                .         .         .         .         .
1651 ACCAGTGCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
     ||||||||||| |||| || || |||||||||||||||||| ||||||||
 737 ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG 786
                .         .         .         .         .
1701 CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
     |||||| |||| || ||| |||| |  || || |||||| |  |||| ||
 787 CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG 836
                .         .         .         .         .
1751 GCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC 1800
     ||||||||| ||||||||  ||||||| ||||||||||||||||  ||||
 837 GCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC 886
                .         .         .         .         .
1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCCAGTGTC 1850
     |||||||||||||| ||| ||  ||||||||||||||| |||||||||||
 887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTC 936
```

FIG. 12E

```
               .         .         .         .         .
1851 CAGTGCAGCCCTGTTCCAGGCCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
     ||||| ||||||  ||||||||||||||||||||| ||| ||||||||||
 937 CAGTGTAGCCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986
               .         .         .         .         .
1901 GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTGCTCTCCGTAC 1950
      ||||||||||||||||| || ||||||||||||||| |||||||||| |
 987 AAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC 1036
               .         .         .         .         .
1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCCAGCCCG 2000
     |||| || || |||||||||||||| || || ||  |||| ||   ||| 
1037 TCTGCAATGGACTGGTGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCC 1086
               .         .         .         .         .
2001 CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT 2050
     ||| |||| |||||| ||||||| |||||||| |||||||||||| || |
1087 CTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT 1136
               .         .         .         .         .
2051 GACGGGCATTTCCTGTGGTCTCCTGGCCTCTGTGGACGCCTTGACCTATG 2100
     ||| |||||||||||||| || || ||||| || || ||| |||||| ||
1137 GACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG 1186
               .         .         .         .         .
2101 GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAG 2150
     |||||||| ||||||| ||||||||||||||||  || || ||||||| |
1187 GTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGG 1236
               .         .         .         .         .
2151 GCTACGGGCTTCCTGGCTGTCCTGGGTTCAGAGGCGTCGGTGCTGCTGCT 2200
     || || ||||||||||| || || || || ||||| ||||||||||||||
1237 GCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTGCT 1286
```

FIG. 12F

```
2201 CACACTGGCGGCCGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT 2250
     ||| ||||| || |||||||||||| |||| ||  |||| ||||| ||||
1287 CACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT 1336

2251 ACGGGAAGGCGCCGTCGCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC 2300
     | |||||| | || || |  |||||||| || ||||| |  || || |||
1337 ATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCCTAGGCTGC 1386

2301 CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCGCTGGCCTCGGTGGGAGA 2350
     ||||| ||||| ||||||||||| ||||||||| ||||||| ||||||||
1387 CTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCTCCCCACTCTGCCTGCCCTACGCCCCACCCGAGGGCCGGC 2400
      || || |||||||||||||||||||||||||| ||||| ||||| | ||
1437 ATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAGC 1486

2401 CGGCCGCCCTGGGCTTCGCTGTAGCCCTGGTGATGATGAACTCGCTCTGC 2450
     | || |||||||||||| | || ||||||||||||||||||||  ||||
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGT 1536

2451 TTCCTGGTGGTGGCCGGCGCCTACATCAAGCTCTACTGTGACCTGCCACG 2500
     |||||||| |||||||| ||||||||||| || |||||||||||||| ||
1537 TTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCG 1586

2501 GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT 2550
     ||| ||||||||||||||||||||||||||||||||| | ||||||||||
1587 GGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCT 1636
```

FIG. 12G

```
2551 GGCTCATCTTTGCAGATGGCCTCCTCTACTGCCCCGTGGCCTTCCTCAGC 2600
     |||||||||| ||||| || ||||||||||| ||||||||||||||||||
1637 GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGC 1686

2601 TTTGCCTCCATGCTGGGCCTCTTCCCTGTCACCCCCGAGGCTGTCAAGTC 2650
     || ||||||||||||||||||||||||||||| |||||||| ||||||||
1687 TTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTC 1736

2651 AGTCCTTCTGGTGGTGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCT 2700
      ||||| |||||||||||||| |||||||||||||||||||||||||| |
1737 TGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGT 1786

2701 ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA 2750
     |||||||||||||||| ||||||||||||||||||||||||||  |||| 
1787 ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCC 1836

2751 AGCCCTCGGTCCCCAGGGCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA 2800
      || |  ||  | | |||||||||||||||| ||||| ||||| ||||||||
1837 CGCGCAGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGA 1886

2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
     |||||||||||| || || ||||| || ||||| || ||||| |||||||
1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936

2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
     |||| ||||||||||||||||| ||||||| ||| |||||||| ||||||
1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACC 1986
```

FIG. 12H

```
2901 TATGGCTTCCCTTCAGTGACCCTCATCTCCCGACATCAGCCGGGGGCCAC 2950
1987 TATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCC 2036

2951 CAGGCTGGAGGGAAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086

3001 ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
2087 ACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136

3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG 3100
2137 ACGCCAGCAGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGG 2186

3101 CTCTCTCTTTGCCTCTCACTTGTAAATATCCCT................. 3133
2187 CTTGGCCTTTGCTTCACACGTGTAAATATCCCTCCCCATTCTTCTCTTCC 2236

3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
2237 CCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286

3175 AAGAAAGACAACTCCAAC............TCCATAGCAAGATGGCCAAC 3212
2287 AACAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAG 2336
```

FIG. 12I

```
3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCTAACCAATGAGTG 3259
2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385

3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTCACCCTG 3306
2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTG 2435

3307 GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
2436 GGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485

3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC 3400
2486 GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG......GGG. 2527

3401 CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
2528 ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568

3450 GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTG 3499
2569 GAGAAAGGC.CTGGAAGGTGATTTCC.........CGTGTGACTC..... 2603

3500 TGACATATAGAATATAAAATGTGTTCTGCGTTCCATTAATCTTGACCTAT 3549
2604 ..ATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATAT 2651
```

FIG. 12J

```
              .         .         .         .         .
3550 GCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA 3599
     ||  :||  ||   |||||| ||||||||  |||||||||| ||| ||||
2652 GCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATTAAAAA 2701

              .         .         .
3600 AAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637
     ||||||||||
2702 AAAAAAAAAA............................ 2711
```

FIG. 13A

```
GAP of: FrGcgManager_102_MTA0uXMaE  check: 8470  from: 1  to: 968

 mLGR6.aa (analysis only) - Import - complete

 to: FrGcgManager_102_NTAf7nCl_  check: 5092  from: 1  to: 737

 corrected hLGR6.aa (analysis onl - Import - complete

 Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
 CompCheck: 1102
  Matrix made by matblas from blosum62.iij

         Gap Weight:      12      Average Match:  2.778
      Length Weight:       4   Average Mismatch: -2.248

            Quality:    3424             Length:    968
              Ratio:   4.646               Gaps:      0
 Percent Similarity:  90.773   Percent Identity: 89.281

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1
```

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_ May 5, 19100 15:04

```
..

                                   .
                                   .
                                   .
                  .         .         .         .         .
 201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
                                        |||||||||||||.|||||
   1 ...............................GLHNLETLDLNYNKLQEFP 19
                  .         .         .         .         .
 251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
     .|||||||||||||||||||||||||||||||||||||||||||||||||
  20 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69
                  .         .         .         .         .
 301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
     |||| |||||||||| |||||||||||||||||||||||||||| |.|||
  70 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119
                  .         .         .         .         .
 351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
     |||||:|||||||||||||||||||||||||.|||| |||||||||| ||
 120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169
                  .         .         .         .         .
 401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
     |||||||||||.||||||||| ||||||||||||||||||||||||||||
 170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219
```

FIG. 13C

```
                   .         .         .         .         .
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
    |||||||||||||||||||||||||||||| ||.|||||| ||||:|||
220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269

                   .         .         .         .         .
501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
    | ::||. |||||||| ||||||| ||||||:  |||||.||||||| ||
270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319

                   .         .         .         .         .
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
    ||||||:||||||||||||||||||||||||||||||| ||.|| ||| |
320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369

                   .         .         .         .         .
601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 650
    |||.|||| ||||||||||||||||:|||.|||||||.||||.|||||||
370 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 419

                   .         .         .         .         .
651 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 700
    ||||||||||||||||||:||.|||||||.|| |||||| ||||||||||
420 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 469

                   .         .         .         .         .
701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 750
    |||||||||||||||||||||||||.|||||| |||||||| ||||||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 519

                   .         .         .         .         .
751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 569
```

FIG. 13D

```
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 850
    ||||||||||||||||||||||||||||||||||||||||| |     ||
570 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 619

851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 900
    ||||||||||||||||||||||||||||||||||||.|||||||||||||
620 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 669

901 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 950
    |||  |||| ||||.| :| :|  |||||| | |||||:|||.| || |
670 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 719

951 SVGGALWPSGSLFASHL* 968
    | ||   |||  ||||.|
720 SGGGGFQPSGLAFASHV* 737
```

FIG. 14A

>15088

> Fbh150881 - Import - vector trimmed

CCGCCSGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCGTGCG
TCCGCGCCCGGCCGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCCAGCCCGCCGGG
GCTCCGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGGCGGCGCCCC
CCAGCCCGGCCCGGGGCCCACCGCCTGCCCGGCCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTTGGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAATCCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGCAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCCTCCCTCCGCCA
CCTCTGGCTGGACGACAATGCACTCACGGAGATCCCTGTCAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGCTGCATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCAGGAACTGGGGTTCCATAA
CAACAACATCAAGGCCATCCCAGAAAAGGCCTTCATGGGGAACCCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTCTCACAATCAAATTGAGGA
GCTGCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAATCGGCCTCCAACACAACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTTCTCCAAGGACAGTTTCCC

FIG. 14B

AAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGGCCTCTGGGCAGTGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAG
CCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCT
GGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGGTGCTGCTGACCGT
GTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGG
CTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCA
GTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCTGGC
CTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGTTTCCTGGT
CGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTA
CTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGA
GGCCGTCAAGTCTGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCT
GTACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGCAGG
GGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTC
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG
GCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCA
GCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACA
CGTGTAAATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCTATAGC

FIG. 14C

AGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTC
CTTGTCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCCTATTAAAATAAGCT
TTGGRAGAGATT

FIG. 15

>15088
MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSF
EGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQHLGTHSFEGLHNLE
TLDLNYNKLQEFPVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAM
DIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFS
QLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVP
YAYQCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFK
PCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEY
GARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEY
GASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVA
FLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQA
LVAFSDVDLILEASEAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGG
GLSGGGGFQPSGLAFASHV*

FIG. 16A

```
protein alignment between mouse and human
> LGR6.

 15088m(analysis only) - Import - complete

 to: FrGcgManager_9_QBAsD4iW_  check: 8637  from: 1  to: 968

 15088h(analysis only) - Import - complete

 Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
 CompCheck: 1102
  Matrix made by matblas from blosum62.iij

         Gap Weight:     12      Average Match:  2.778
      Length Weight:      4   Average Mismatch: -2.248

            Quality:   4495             Length:    968
              Ratio:  4.653               Gaps:      2
 Percent Similarity: 91.097   Percent Identity: 89.855

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   2
                   . =   1

 FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24
..
```

FIG. 16B

```
  1 MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA  50   Mouse
    | ||||| |||||| |||| | |  ||||||  |||||||||||||||||
  1 MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA  50   Human

 51 DCSELGLSVVPADLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100
    |||||||| || ||||||||||||||||||||||||||||||||||||||
 51 DCSELGLSAVPGDLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100

101 HLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLI 150
    |||||||||||||:||||||||.||| |||||||||||||||||||||||
101 HLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLI 150

151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRH 200
    |||||||||||||||||||||||||||||||||||||||||||||| | |
151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISH 200

201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
    ||||||||||||||||||||||||.|||.|||||||| ||||||.|||||
201 IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEFP 250

251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
    .|||||||||||||||||||||||||||||||||||||||||||||||||
251 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300

301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
    |||| |||||||||| |||||||||||||||||||||||||||| |.|||
301 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 350
```

FIG. 16C

```
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
    |||||:|||||||||||||||||||||||||.|||| |||||||||| ||
351 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 400

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
    |||||||||||.||||||||| ||||||||||||||||||||||||||||
401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
    |||||||||||||||||||||||||||||| ||.|||||| ||||:|||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 500

501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
    | ::||. |||||||| ||||||| ||||||:  |||||.||||||| ||
501 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 550

551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV 598
    ||||||:||||||||||||||||||||||| ||||||| ||.|| | | |
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 600

599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
    |||.|||| ||||||||||||||||:|||.|||||||.||||.|||||||
601 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 650

649 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 698
    ||||||||||||||||||:||.|||||||.|| |||||| ||||||||||
651 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 700
```

FIG. 16D

```
             .         .         .         .         .
699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 748
    |||||||||||||||||||||||||.|||||| |||||||| ||||||||
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 750

             .         .         .         .         .
749 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 798
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800

             .         .         .         .         .
799 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 848
    ||||||||||||||||||||||||||||||||||||||||| |     ||
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 850

             .         .         .         .         .
849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
    ||||||||||||||||||||||||||||||||||||.|||||||||||||
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900

             .         .         .         .         .
899 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 948
    |||  |||| ||||.| :| :|  |||||| | |||||:|||.| || | 
901 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 950

             .
949 SVGGALWPSGSLFASHL* 966
    | ||   |||  ||||.|
951 SGGGGFQPSGLAFASHV* 968
```